

I. AMENDMENTS

A. In the Specification

Please amend the Title of the application at page 1 and page 142, as follows:

USE OF FOLLISTATIN TO INCREASE MUSCLE MASS TRANSGENIC NON-HUMAN
ANIMALS EXPRESSING A TRUNCATED ACTIVIN TYPE II RECEPTOR

Please amend the following paragraphs of the specification, as indicated:

[0035] A number of genome databases are available for comparison, including, for example, a substantial portion of the human genome is available as part of the Human Genome Sequencing Project (J. Roach, at hypertext transfer protocol ("http"), URL "weber.u.Washington.edu/~roach/human_genome_progress2.html" http://weber.u.Washington.edu/~roach/human_genome_progress2.html). In addition, at least twenty-one genomes have been sequenced in their entirety, including, for example, *M. genitalium*, *M. jannaschii*, *H. influenzae*, *E. coli*, yeast (*S. cerevisiae*), and *D. melanogaster*. Significant progress has also been made in sequencing the genomes of model organism such as mouse, *C. elegans*, and *Arabidopsis* sp. Several databases containing genomic information annotated with some functional information are maintained by different organizations, and are accessible via the internet, for example, at http, URL "www.tigr.org/tdb"; at http, on the world wide web ("www"), at URL "genetics.wisc.edu"; at http, URL "[genome-www.stanford.edu/~ball](http://www.stanford.edu/~ball)"; at http "hiv-web.lanl.gov"; at http, on the www, at URL "ncbi.nlm.nih.gov"; at http, on the www, at URL "ebi.ac.uk"; at http, URL "Pasteur.fr/other/biology"; and at http, on the www, at URL "genome.wi.mit.edu"; <http://www.tigr.org/tdb>; <http://www.genetics.wisc.edu>; <http://genome-www.stanford.edu/~ball>; <http://hiv-web.lanl.gov>; <http://www.ncbi.nlm.nih.gov>; <http://www.ebi.ac.uk>; <http://Pasteur.fr/other/biology>; and <http://www.genome.wi.mit.edu>.

In re Application of
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[0036] One example of a useful algorithm is BLAST and BLAST 2.0 algorithms, which are described by Altschul et al. (Nucleic Acids Res. 25:3389-3402, 1997; J. Mol. Biol. 215:403-410, 1990, each of which is incorporated herein by reference). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (at <http://www.ncbi.nlm.nih.gov>).

[0039] The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (i.e., aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet et al., Science 256:1443-1445, 1992; Henikoff and Henikoff, Proteins 17:49-61, 1993, each of which is incorporated herein by reference). Less preferably, the PAM or PAM250 matrices may also be used (Schwartz and Dayhoff, eds., "Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure" (Washington, National Biomedical Research Foundation 1978)). BLAST programs are accessible through the U.S. National Library of Medicine, for example, at <http://www.ncbi.nlm.nih.gov> <http://www.ncbi.nlm.nih.gov>.